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U.S. APPLICATION NUMBER NO.	FIRST NAMED APPLICANT	ATTY. DOCKET NO.
10/566,944	Thorsten Zank	12810-00193-US
INTERNATIONAL APPLICATION NO.		
PCT/EP04/07957		
I.A. FILING DATE	PRIORITY DATE	
07/16/2004	08/01/2003	

23416
 CONNOLLY BOVE LODGE & HUTZ, LLP
 P O BOX 2207
 WILMINGTON, DE 19899

CONFIRMATION NO. 5346
371 FORMALITIES LETTER

OC00000023991140

Date Mailed: 05/22/2007

**NOTIFICATION TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS
 CONTAINING NUCLEOTIDE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

Applicant is given **TWO MONTHS FROM THE DATE OF THIS NOTICE** within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

Applicant is cautioned that correction of the above items may cause the specification and drawings page count to exceed 100 pages. If the specification and drawings exceed 100 pages, applicant will need to submit the required application size fee.

For questions regarding compliance to 37 CFR 1.821-1.825 requirements, please contact:

- **For Rules Interpretation, call (571) 272-0951**
- **For Patentin Software Program Help, call Patent EBC at 1-866-217-9197 or directly at 703-305-3028 / 703-308-6845 between the hours of 6 a.m. and 12 midnight, Monday through Friday, EST.**
- **Send e-mail correspondence for Patentin Software Program Help @ ebc@uspto.gov**

Applicant is reminded that any communications to the United States Patent and Trademark Office must be mailed to the address given in the heading and include the U.S. application no. shown above (37 CFR 1.5)

Registered users of EFS-Web may alternatively submit their reply to this notice via EFS-Web.
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If you are not using EFS-Web to submit your reply, you must include a copy of this notice.

KAREN R MCLEAN

Telephone: (703) 308-9140 EXT 214

PART 1 - ATTORNEY/APPLICANT COPY

U.S. APPLICATION NUMBER NO.	INTERNATIONAL APPLICATION NO.	ATTY. DOCKET NO.
10/566,944	PCT/EP04/07957	12810-00193-US

FORM PCT/DO/EO/922 (371 Formalities Notice)

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/566,944
Source: JFWP
Date Processed by STIC: 02/14/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

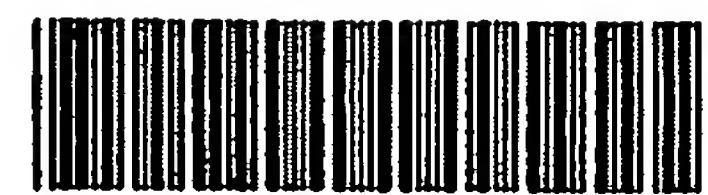
Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED
SUGGESTED CORRECTION
SERIAL NUMBER: 10/566,944

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1	____ Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2	____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3	____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4	____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5	____ Variable Length	Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6	____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7	____ Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8	____ Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9	____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10	____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11	____ Use of <220>	Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12	____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13	____ Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/566,944

DATE: 02/14/2006

TIME: 12:55:17

Input Set : F:\Sequence listing (12810-00193-US).txt
 Output Set: N:\CRF4\02142006\J566944.raw

3 <110> APPLICANT: Zank, Thorsten
 4 Bauer, Jorg
 5 Cirpus, Petra
 6 Abbadie, Amine
 7 Heinz, Ernst
 8 Qiu, Xiao
 9 Vrinten, Patricia
 10 Sperling, Petra
 11 Domergue, Frederic
 12 Meyer, Astrid
 13 Kirsch, Jelena

15 <120> TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF MULTIPLE-UNSATURATED FATTY ACIDS IN

16 TRANSGENIC ORGANISMS
 18 <130> FILE REFERENCE: 12810-00193-US
 >>> 20 <140> CURRENT APPLICATION NUMBER: US/10/566,944
 >>> 20 <141> CURRENT FILING DATE: 2006-02-01
 20 <150> PRIOR APPLICATION NUMBER: DE 103 35 992.3
 21 <151> PRIOR FILING DATE: 2003-08-01
 23 <150> PRIOR APPLICATION NUMBER: DE 103 44 557.9
 24 <151> PRIOR FILING DATE: 2003-09-24
 26 <150> PRIOR APPLICATION NUMBER: DE 103 47 869.8
 27 <151> PRIOR FILING DATE: 2003-10-10
 29 <150> PRIOR APPLICATION NUMBER: DE 103 59 593.7
 30 <151> PRIOR FILING DATE: 2003-12-18
 32 <150> PRIOR APPLICATION NUMBER: DE 10 2004 009 457.8
 33 <151> PRIOR FILING DATE: 2004-02-27
 35 <150> PRIOR APPLICATION NUMBER: DE 10 2004 012 370.5
 36 <151> PRIOR FILING DATE: 2004-03-13
 38 <150> PRIOR APPLICATION NUMBER: DE 10 2004 024 014.0
 39 <151> PRIOR FILING DATE: 2004-05-14
 41 <160> NUMBER OF SEQ ID NOS: 192
 43 <170> SOFTWARE: PatentIn version 3.1
 46 <210> SEQ ID NO: 1
 47 <211> LENGTH: 1266
 48 <212> TYPE: DNA
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48

RAW SEQUENCE LISTING
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DATE: 02/14/2006
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62	Tyr	Asp	Val	Ser	Ala	Trp	Val	Asn	Phe	His	Pro	Gly	Gly	Ala	Glu	Ile	
63								20		25		30					
65	ata	gag	aat	tac	caa	gga	agg	gat	gcc	act	gat	gcc	ttc	atg	gtt	atg	144
66	Ile	Glu	Asn	Tyr	Gln	Gly	Arg	Asp	Ala	Thr	Asp	Ala	Phe	Met	Val	Met	
68								35		40		45					
70	cac	tct	caa	gaa	gcc	ttc	gac	aag	ctc	aag	cgc	atg	ccc	aaa	atc	aat	192
71	His	Ser	Gln	Glu	Ala	Phe	Asp	Lys	Leu	Lys	Arg	Met	Pro	Lys	Ile	Asn	
72								50		55		60					
74	ccc	agt	tct	gag	ttg	cca	ccc	cag	gct	gca	gtg	aat	gaa	gct	caa	gag	240
75	Pro	Ser	Ser	Glu	Leu	Pro	Pro	Gln	Ala	Ala	Val	Asn	Glu	Ala	Gln	Glu	
76	65						70			75		80					
78	gat	ttc	cgg	aag	ctc	cga	gaa	gag	ttg	atc	gca	act	ggc	atg	ttt	gat	288
79	Asp	Phe	Arg	Lys	Leu	Arg	Glu	Glu	Leu	Ile	Ala	Thr	Gly	Met	Phe	Asp	
80							85			90		95					
82	gcc	tcc	ccc	ctc	tgg	tac	tca	tac	aaa	atc	agc	acc	aca	ctg	ggc	ctt	336
83	Ala	Ser	Pro	Leu	Trp	Tyr	Ser	Tyr	Lys	Ile	Ser	Thr	Thr	Leu	Gly	Leu	
84							100			105		110					
86	gga	gtg	ctg	ggt	tat	ttc	ctg	atg	gtt	cag	tat	cag	atg	tat	ttc	att	384
87	Gly	Val	Leu	Gly	Tyr	Phe	Leu	Met	Val	Gln	Tyr	Gln	Met	Tyr	Phe	Ile	
88							115			120		125					
90	ggg	gca	gtg	ttg	ctt	ggg	atg	cac	tat	caa	cag	atg	ggc	tgg	ctt	tct	432
91	Gly	Ala	Val	Leu	Leu	Gly	Met	His	Tyr	Gln	Gln	Met	Gly	Trp	Leu	Ser	
92							130			135		140					
94	cat	gac	att	tgc	cac	cac	cag	act	ttc	aag	aac	cgg	aac	tgg	aac	aac	480
95	His	Asp	Ile	Cys	His	His	Gln	Thr	Phe	Lys	Asn	Arg	Asn	Trp	Asn	Asn	
96	145						150			155		160					
98	ctc	gtg	gga	ctg	gta	ttt	ggc	aat	ggt	ctg	caa	ggt	ttt	tcc	gtg	aca	528
99	Leu	Val	Gly	Leu	Val	Phe	Gly	Asn	Gly	Leu	Gln	Gly	Phe	Ser	Val	Thr	
101							165			170		175					
103	tgc	tgg	aag	gac	aga	cac	aat	gca	cat	cat	tcg	gca	acc	aat	gtt	caa	576
104	Cys	Trp	Lys	Asp	Arg	His	Asn	Ala	His	His	Ser	Ala	Thr	Asn	Val	Gln	
105							180			185		190					
107	ggg	cac	gac	cct	gat	att	gac	aac	ctc	ccc	ctc	tta	gcc	tgg	tct	gag	624
108	Gly	His	Asp	Pro	Asp	Ile	Asp	Asn	Leu	Pro	Leu	Leu	Ala	Trp	Ser	Glu	
109							195			200		205					
111	gat	gac	gtc	aca	cgg	gct	tca	ccg	att	tcc	cgc	aag	ctc	att	cag	ttc	672
112	Asp	Asp	Val	Thr	Arg	Ala	Ser	Pro	Ile	Ser	Arg	Lys	Leu	Ile	Gln	Phe	
113							210			215		220					
115	cag	cag	tat	tat	ttc	ttg	gtc	atc	tgt	atc	ttg	ttg	cggt	ttc	att	tgg	720
116	Gln	Gln	Tyr	Tyr	Phe	Leu	Val	Ile	Cys	Ile	Leu	Leu	Arg	Phe	Ile	Trp	
117	225						230			235		240					
119	tgt	ttc	cag	agc	gtg	ttg	acc	gtg	cgc	agt	ctg	aag	gac	aga	gat	aac	768
120	Cys	Phe	Gln	Ser	Val	Leu	Thr	Val	Arg	Ser	Leu	Lys	Asp	Arg	Asp	Asn	
121							245			250		255					
123	caa	ttc	tat	cgc	tct	cag	tat	aag	aag	gag	gcc	att	ggc	ctc	gcc	ctg	816
124	Gln	Phe	Tyr	Arg	Ser	Gln	Tyr	Lys	Lys	Glu	Ala	Ile	Gly	Leu	Ala	Leu	
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PATENT APPLICATION: US/10/566,944

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129	275 280 285	
131	ctc aca tcg ctg ttg gta ttt ttc gtt tcg gag ctg gtt ggc ggc ttc	912
132	Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe	
135	290 295 300	
137	ggc att gcg atc gtg gtg ttc atg aac cac tac cca ctg gag aag atc	960
138	Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile	
139	305 310 315 320	
141	ggg gac tcg gtc tgg gat ggc cat gga ttc tcg gtt ggc cag atc cat	1008
142	Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His	
143	325 330 335	
145	gag acc atg aac att cgg cga ggg att atc aca gat tgg ttt ttc gga	1056
146	Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly	
147	340 345 350	
149	ggc ttg aac tac cag atc gag cac cat ttg tgg ccg acc ctc cct cgc	1104
150	Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg	
151	355 360 365	
153	cac aac ctg aca gcg gtt agc tac cag gtg gaa cag ctg tgc cag aag	1152
154	His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys	
155	370 375 380	
157	cac aac ctg ccg tat cgg aac ccg ctg ccc cat gaa ggg ttg gtc atc	1200
158	His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile	
159	385 390 395 400	
161	ctg ctg cgc tat ctg gcg gtg ttc gcc ccg atg gcg gag aag caa ccc	1248
162	Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro	
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183	20 25 30	
186	Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met	
187	35 40 45	
190	His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn	
191	50 55 60	
194	Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu	
195	65 70 75 80	
198	Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp	
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211      130          135          140
214 His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn
215 145          150          155          160
218 Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr
219      165          170          175
222 Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln
223      180          185          190
226 Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu
227      195          200          205
230 Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe
231 210          215          220
234 Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp
235 225          230          235          240
238 Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn
239      245          250          255
242 Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu
243      260          265          270
246 His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile
247      275          280          285
250 Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe
251 290          295          300
254 Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile
255 305          310          315          320
258 Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His
259      325          330          335
262 Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly
263      340          345          350
266 Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg
267      355          360          365
270 His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys
271 370          375          380
274 His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile
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289 <213> ORGANISM: Isochrysis galbana
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293 <222> LOCATION: (1)..(777)
294 <223> OTHER INFORMATION: delta9-elongase
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/566,944

DATE: 02/14/2006
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302 Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Lys Pro	
303 20 25 30	
305 ctg ctc cgc aat tcc ggg ctg gtg gat gag aag aag ggc gca tac agg	144
306 Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg	
307 35 40 45	
309 acg tcc atg atc tgg tac aac gtt ctg ctg gcg ctc ttc tct gcg ctg	192
310 Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu	
311 50 55 60	
313 agc ttc tac gtg acg gcg acc gcc ctc ggc tgg gac tat ggt acg ggc	240
314 Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly	
315 65 70 75 80	
317 gcg tgg ctg cgc agg caa acc ggc gac aca ccg cag ccg ctc ttc cag	288
318 Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln	
319 85 90 95	
321 tgc ccg tcc ccg gtt tgg gac tcg aag ctc ttc aca tgg acc gcc aag	336
322 Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys	
323 100 105 110	
325 gca ttc tat tac tcc aag tac gtg gag tac ctc gac acg gcc tgg ctg	384
326 Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu	
327 115 120 125	
329 agg gtc tcc ttt ctc cag gcc ttc cac cac ttt ggc gcg ccg tgg gat	432
330 Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp	
331 130 135 140	
333 gtg tac ctc ggc att cgg ctg cac aac gag ggc gta tgg atc ttc atg	480
334 Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met	
335 145 150 155 160	
337 ttt ttc aac tcg ttc att cac acc atc atg tac acc tac tac ggc ctc	528
338 Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Gly Leu	
339 165 170 175	
341 acc gcc gcc ggg tat aag ttc aag gcc aag ccg ctc atc acc gcg atg	576
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343 180 185 190	
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346 Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile	
347 195 200 205	
349 aac gtc ccc tgc ttc aac tcg gac aaa ggg aag ttg ttc agc tgg gct	672
350 Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala	
351 210 215 220	
353 ttc aac tat gca tac gtc ggc tcg gtc ttc ttg ctc ttc tgc cac ttt	720
354 Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe	
355 225 230 235 240	
357 ttc tac cag gac aac ttg gca acg aag aaa tcg gcc aag gcg ggc aag	768
358 Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser Ala Lys Ala Gly Lys	
359 245 250 255	
361 cag ctc tag	777

<210> SEQ ID NO 115
 <211> LENGTH: 13
 <212> TYPE: PRT
 <213> ORGANISM: Unknown
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (1)..(13)
 <223> OTHER INFORMATION: Xaa in the sequence at position 2, 3, 4, 6, 7, 8 and 9
 has the meaning given in Table A.
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (1)..(13)
 <223> OTHER INFORMATION: Consensus
 <400> SEQUENCE: 115

Asn Xaa Xaa Xaa His Xaa Xaa Met Tyr Xaa Tyr Tyr Xaa

1

5

10

→ Invalid Response. 'Xaa' Represents
 single Amino Acid. Pls see Item
 # 9 in Error
 Summary Sheet.

Tyr at this
location

Xaa
?

1

FYI

The type of errors shown exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/566,944

DATE: 02/14/2006
TIME: 12:55:18

Input Set : F:\Sequence listing (12810-00193-US).txt
Output Set: N:\CRF4\02142006\J566944.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:115; Xaa Pos. 2,3,4,6,7,10,13
Seq#:116; Xaa Pos. 3,4,5,6
Seq#:139; Xaa Pos. 3,4
Seq#:140; Xaa Pos. 2,3,5,6
Seq#:141; Xaa Pos. 3
Seq#:142; Xaa Pos. 5,6
Seq#:185; N Pos. 3,18
Seq#:186; N Pos. 3,9,12,15,21

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:115; Line(s) 12392
Seq#:116; Line(s) 12415
Seq#:140; Line(s) 13593
Seq#:142; Line(s) 13635

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/566,944

DATE: 02/14/2006
TIME: 12:55:18

Input Set : F:\Sequence listing (12810-00193-US).txt
Output Set: N:\CRF4\02142006\J566944.raw

L:20 M:270 C: Current Application Number differs, Replaced Current Application No
L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:12403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:115 after pos.:0
L:12426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:116 after pos.:0
L:13581 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:139 after pos.:0
L:13602 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:140 after pos.:0
L:13623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:141 after pos.:0
L:13646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:142 after pos.:0
L:14407 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:185 after pos.:0
L:14426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:186 after pos.:0